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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/770,509

DATE: 02/06/2001
 TIME: 15:23:09

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\02062001\I770509.raw

4 <110> APPLICANT: Katagiri, F.
 6 <120> TITLE OF INVENTION: OOMYCETE FTSZ-MT AS A TARGET FOR
 7 ANTIMICROBIAL-SPECIFIC BIOCIDES
 10 <130> FILE REFERENCE: NADII.018A
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/770,509
 C--> 12 <141> CURRENT FILING DATE: 2001-01-25
 12 <160> NUMBER OF SEQ ID NOS: 32
 14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 535
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Phytophthora infestans
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (2)...(535)
 25 <400> SEQUENCE: 1
 26 c gcg tcg caa ttg gaa ggt gtg gag ttc att gta gcc aac aca gac tgt 49
 27 Ala Ser Gln Leu Glu Gly Val Glu Phe Ile Val Ala Asn Thr Asp Cys
 28 1 5 10 15
 30 cag gct ctg gga cgc tcg ctg gcg ccg cac aag atc acg ctg ggc aaa 97
 31 Gln Ala Leu Gly Arg Ser Leu Ala Pro His Lys Ile Thr Leu Gly Lys
 32 20 25 30
 34 gat atc acc aag gga cta gga gct gga tcc aaa cct gag ctg ggt aaa 145
 35 Asp Ile Thr Lys Gly Leu Gly Ala Gly Ser Lys Pro Glu Leu Gly Lys
 36 35 40 45
 38 cgc tct gcg gaa cag cag aaa gtg gat atc caa cgg atg tta cag gac 193
 39 Arg Ser Ala Glu Gln Gln Lys Val Asp Ile Gln Arg Met Leu Gln Asp
 40 50 55 60
 42 agc aac atg ctg ttt atc acg ggc gga atg ggc ggc gga acc tgc aca 241
 43 Ser Asn Met Leu Phe Ile Thr Gly Gly Met Gly Gly Gly Thr Cys Thr
 44 65 70 75 80
 46 gga gcc gca cct gtc gtg gcc agt gta gcc agg gag ctg ggg atc cta 289
 47 Gly Ala Ala Pro Val Val Ala Ser Val Ala Arg Glu Leu Gly Ile Leu
 48 85 90 95
 50 acg gtc gga gta gta agc aca ccg ttc cga tcc gaa gga ccc aat cgc 337
 51 Thr Val Gly Val Val Ser Thr Pro Phe Arg Ser Glu Gly Pro Asn Arg
 52 100 105 110
 54 act cgt ctg gcc aat gct gga gta aaa gaa ctg gcc aag tac gtc gac 385
 55 Thr Arg Leu Ala Asn Ala Gly Val Lys Glu Leu Ala Lys Tyr Val Asp
 56 115 120 125
 58 acc tta att gtc gtg ccc aac cag aac ttg ctg gct ttg gca gac aag 433
 59 Thr Leu Ile Val Val Pro Asn Gln Asn Leu Leu Ala Leu Ala Asp Lys
 60 130 135 140
 62 agc acg acc atg ttg gaa gcc ttc cgg tat gcc gac gac gtg ctg ctt 481
 63 Ser Thr Thr Met Leu Glu Ala Phe Arg Tyr Ala Asp Asp Val Leu Leu
 64 145 150 155 160
 66 gaa gga gtt aaa ggt gtc acg gac ttg atc gtt cgc ccg gga ctt atc 529

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67 Glu Gly Val Lys Gly Val Thr Asp Leu Ile Val Arg Pro Gly Leu Ile
68           165           170           175
70 aat ttg
71 Asn Leu
75 <210> SEQ ID NO: 2
76 <211> LENGTH: 178
77 <212> TYPE: PRT
78 <213> ORGANISM: Phytophthora infestans
80 <400> SEQUENCE: 2
81 Ala Ser Gln Leu Glu Gly Val Glu Phe Ile Val Ala Asn Thr Asp Cys
82 1           5           10           15
83 Gln Ala Leu Gly Arg Ser Leu Ala Pro His Lys Ile Thr Leu Gly Lys
84           20           25           30
85 Asp Ile Thr Lys Gly Leu Gly Ala Gly Ser Lys Pro Glu Leu Gly Lys
86           35           40           45
87 Arg Ser Ala Glu Gln Gln Lys Val Asp Ile Gln Arg Met Leu Gln Asp
88           50           55           60
89 Ser Asn Met Leu Phe Ile Thr Gly Gly Met Gly Gly Gly Thr Cys Thr
90 65           70           75           80
91 Gly Ala Ala Pro Val Val Ala Ser Val Ala Arg Glu Leu Gly Ile Leu
92           85           90           95
93 Thr Val Gly Val Val Ser Thr Pro Phe Arg Ser Glu Gly Pro Asn Arg
94           100          105          110
95 Thr Arg Leu Ala Asn Ala Gly Val Lys Glu Leu Ala Lys Tyr Val Asp
96           115          120          125
97 Thr Leu Ile Val Val Pro Asn Gln Asn Leu Leu Ala Leu Ala Asp Lys
98           130          135          140
99 Ser Thr Thr Met Leu Glu Ala Phe Arg Tyr Ala Asp Asp Val Leu Leu
100 145          150          155          160
101 Glu Gly Val Lys Gly Val Thr Asp Leu Ile Val Arg Pro Gly Leu Ile
102           165          170          175
103 Asn Leu
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 220
109 <212> TYPE: DNA
110 <213> ORGANISM: Phytophthora infestans
112 <220> FEATURE:
113 <221> NAME/KEY: CDS
114 <222> LOCATION: (2)...(220)
115 <223> OTHER INFORMATION: cDNA
117 <400> SEQUENCE: 3
118 c gcg cgc ggc ctg cag ggt gtg gag ttt ctt gtt tgc aac acg gat gct 49
119 Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala
120 1           5           10           15
122 cag cac tta cgc acg acg ctg acg gag aac cgc gtt cag atg gct cct 97
123 Gln His Leu Arg Thr Thr Leu Thr Glu Asn Arg Val Gln Met Ala Pro
124           20           25           30
126 gaa ttg act gga gga ttg ggc tgt ggc gct aac ccc gaa gtt ggc cga 145
127 Glu Leu Thr Gly Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly Arg

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```

128          35          40          45
130 gag gcg gca gag gcc gcg att gat gag att ttg gag cgc gtt cag ggt 193
131 Glu Ala Ala Glu Ala Ala Ile Asp Glu Ile Leu Glu Arg Val Gln Gly
132          50          55          60
134 gca aac atg atg ttt gtt act gcg ggt 220
135 Ala Asn Met Met Phe Val Thr Ala Gly
136 65          70
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 73
141 <212> TYPE: PRT
142 <213> ORGANISM: Phytophthora infestans
144 <400> SEQUENCE: 4
145 Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala
146 1          5          10          15
147 Gln His Leu Arg Thr Thr Leu Thr Glu Asn Arg Val Gln Met Ala Pro
148          20          25          30
149 Glu Leu Thr Gly Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly Arg
150          35          40          45
151 Glu Ala Ala Glu Ala Ala Ile Asp Glu Ile Leu Glu Arg Val Gln Gly
152          50          55          60
153 Ala Asn Met Met Phe Val Thr Ala Gly
154 65          70
157 <210> SEQ ID NO: 5
158 <211> LENGTH: 388
159 <212> TYPE: DNA
160 <213> ORGANISM: Phytophthora infestans
162 <220> FEATURE:
163 <221> NAME/KEY: intron
164 <222> LOCATION: (143)...(204)
166 <221> NAME/KEY: intron
167 <222> LOCATION: (265)...(370)
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (2)...(142)
172 <221> NAME/KEY: CDS
173 <222> LOCATION: (205)...(264)
175 <221> NAME/KEY: CDS
176 <222> LOCATION: (371)...(388)
178 <400> SEQUENCE: 5
179 c gcg cgc gcc ctg cag ggt gtg gag ttt ctt gtt tgc aac acg gat gct 49
180 Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala
181 1          5          10          15
183 cag cac tta cgc acg acg ctg acg gag aac cgc gtt cag atg gct cct 97
184 Gln His Leu Arg Thr Thr Leu Thr Glu Asn Arg Val Gln Met Ala Pro
185          20          25          30
187 gaa ttg act gga gga ttg ggc tgt ggc gct aac ccc gaa gtt ggg 142
188 Glu Leu Thr Gly Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly
189          35          40          45
191 tgagtgactg cgtaaaagcg gtattttttt ttcttacata ctgaccttaa ctattgatta 202
192 gc cga gag gcg gca gag gcc gcg att gat gag att ttg gag cgc gtt 249

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```

193   Arg Glu Ala Ala Glu Ala Ala Ile Asp Glu Ile Leu Glu Arg Val
194           50                               55                               60
196   cag ggt gca aac atg gttgtctcg gtgacattgc gtttctcaag acgttccgat   304
197   Gln Gly Ala Asn Met
198           65
200   ttgagcgaat gacttgggtga tgacaacgat atgattatta acttctgctt ttatgccccct 364
201   atatag atg ttt gtt act gcg ggt                                     388
202           Met Phe Val Thr Ala Gly
203           70
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: PCR primer
215 <221> NAME/KEY: misc_feature
216 <222> LOCATION: (1)...(20)
217 <223> OTHER INFORMATION: n = inosine
219 <400> SEQUENCE: 6
W--> 220 aaygcngtna ayaayatgat                                     20
222 <210> SEQ ID NO: 7
223 <211> LENGTH: 20
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: PCR primer
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: (1)...(20)
233 <223> OTHER INFORMATION: n = inosine
235 <400> SEQUENCE: 7
W--> 236 gtnccngtnc cncnccccat                                     20
238 <210> SEQ ID NO: 8
239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: PCR primer
247 <221> NAME/KEY: misc_feature
248 <222> LOCATION: (1)...(17)
249 <223> OTHER INFORMATION: n = inosine
251 <400> SEQUENCE: 8
W--> 252 gtncknacrt cngcraartc                                     20
254 <210> SEQ ID NO: 9
255 <211> LENGTH: 1423
256 <212> TYPE: DNA
257 <213> ORGANISM: Phytophthora infestans
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (2)...(1261)

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263 <400> SEQUENCE: 9
264 g atg gcg ata tcc cgc atg aaa gct gcg gcg atg gcg ctg cta cgt gcc 49
265 Met Ala Ile Ser Arg Met Lys Ala Ala Ala Met Ala Leu Leu Arg Ala
266 1 5 10 15
268 cgc cag acc tcc cag tcc gcc act caa cac ctc gcc ttc tct act gaa 97
269 Arg Gln Thr Ser Gln Ser Ala Thr Gln His Leu Ala Phe Ser Thr Glu
270 20 25 30
272 gcc act gat gct gca gct gcc gcg tta cgc atg ggc ttt aaa aag gct 145
273 Ala Thr Asp Ala Ala Ala Ala Ala Leu Arg Met Gly Phe Lys Lys Ala
274 35 40 45
276 cga aaa gac gag gat ggc ggt gtg aaa gtg ggg ctg gag gca gag ccc 193
277 Arg Lys Asp Glu Asp Gly Gly Val Lys Val Gly Leu Glu Ala Glu Pro
278 50 55 60
280 gat tca cca aca gat gtg agc gcc gtt tcg acg cca gta gta gag aag 241
281 Asp Ser Pro Thr Asp Val Ser Ala Val Ser Thr Pro Val Val Glu Lys
282 65 70 75 80
284 aag ctc gtg ccg cca gcc atg agc tcc aca cag cca ctt tgg ctc aca 289
285 Lys Leu Val Pro Pro Ala Met Ser Ser Thr Gln Pro Leu Trp Leu Thr
286 85 90 95
288 cag gac cat cct gtg aca gac ctg tcg ggc ttt gca ccg aag att gtg 337
289 Gln Asp His Pro Val Thr Asp Leu Ser Gly Phe Ala Pro Lys Ile Val
290 100 105 110
292 gtg gtt ggc gtc gga gga gct gga gga aat gcg gtg aac aac atg atc 385
293 Val Val Gly Val Gly Gly Ala Gly Gly Asn Ala Val Asn Asn Met Ile
294 115 120 125
296 gcg cgc ggc ctg cag ggt gtg gag ttt ctt gtt tgc aac acg gat gct 433
297 Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala
298 130 135 140
300 cag cac tta cgc acg acg ctg acg gag aac cgc gtt cag atg gct cct 481
301 Gln His Leu Arg Thr Thr Leu Thr Glu Asn Arg Val Gln Met Ala Pro
302 145 150 155 160
304 gaa ttg act gga gga ctg ggc tgt ggc gct aac ccc gaa gtt ggc cga 529
305 Glu Leu Thr Gly Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly Arg
306 165 170 175
308 gag gcg gca gag gcc gcg att gat gag att ttg gag cgc gtt cag ggt 577
309 Glu Ala Ala Glu Ala Ala Ile Asp Glu Ile Leu Glu Arg Val Gln Gly
310 180 185 190
312 gca aac atg atg ttt gtt act gcg ggt atg ggt ggc gga aca ggt aca 625
313 Ala Asn Met Met Phe Val Thr Ala Gly Met Gly Gly Gly Thr Gly Thr
314 195 200 205
316 ggt gca gca ccc gtc att gct cag gct gcc tta gat gct ggt atc ctc 673
317 Gly Ala Ala Pro Val Ile Ala Gln Ala Ala Leu Asp Ala Gly Ile Leu
318 210 215 220
320 acc gta gct gtc gtt act aag ccg ttc cgg ttt gag gga aac aac cgt 721
321 Thr Val Ala Val Val Thr Lys Pro Phe Arg Phe Glu Gly Asn Asn Arg
322 225 230 235 240
324 gca aag ctt gcg gca caa ggc ctc gct gaa ctg aag gat agc gtc gat 769
325 Ala Lys Leu Ala Ala Gln Gly Leu Ala Glu Leu Lys Asp Ser Val Asp
326 245 250 255

```

VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\02062001\I770509.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8